Online-Only Abstracts

The microbiological diagnosis of tuberculous meningitis: results of Haydarpasa-1 study

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Abstract

We aimed to provide data on the diagnosis of tuberculous meningitis (TBM) in this largest case series ever reported. The Haydarpasa-1 study involved patients with microbiologically confirmed TBM in Albania, Croatia, Denmark, Egypt, France, Hungary, Iraq, Italy, Macedonia, Romania, Serbia, Slovenia, Syria and Turkey between 2000 and 2012. A positive culture, PCR or Ehrlich–Ziehl–Neelsen staining (EZNs) from the cerebrospinal fluid (CSF) was mandatory for inclusion of meningitis patients. A total of 506 TBM patients were included. The sensitivities of the tests were as follows: interferon-γ release assay (Quantiferon TB gold in tube) 90.2%, automated culture systems (ACS) 81.8%, Löwenstein Jensen medium (L-J) 72.7%, adenosine deaminase (ADA) 29.9% and EZNs 27.3%. CSF-ACS was superior to CSF L-J culture and CSF-PCR ($p < 0.05$ for both). Accordingly, CSF L-J culture was superior to CSF-PCR ($p < 0.05$). Combination of L-J and ACS was superior to using these tests alone ($p < 0.05$). There were poor and inverse agreements between EZNs and L-J culture ($\kappa = -0.189$); ACS and L-J culture ($\kappa = -0.172$) ($p < 0.05$ for both). Fair and inverse agreement was detected for CSF-ADA and CSF-PCR ($\kappa = -0.299$, $p < 0.05$). Diagnostic accuracy of TBM was increased when both ACS and L-J cultures were used together. Non-culture tests contributed to TBM diagnosis to a degree. However, due to the delays in the diagnosis with any of the cultures, combined use of non-culture tests appears to contribute early diagnosis. Hence, the diagnostic approach to TBM should be individualized according to the technical capacities of medical institutions particularly in those with poor resources.

Genome sequencing and characterization of an extensively drug-resistant sequence type 111 serotype O12 hospital outbreak strain of *Pseudomonas aeruginosa*

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Abstract

A series of extensively drug-resistant isolates of *Pseudomonas aeruginosa* from two outbreaks in UK hospitals were characterized by whole genome sequencing (WGS). Although these isolates were resistant to antibiotics other than colistin, we confirmed that they are still sensitive to disinfectants. The sequencing confirmed that isolates in the larger outbreak were serotype O12, and also revealed that they belonged to sequence type ST111, which is a major epidemic strain of *P. aeruginosa* throughout Europe. As this is the first reported

sequence of an ST111 strain, the genome was examined in depth, focusing particularly on antibiotic resistance and potential virulence genes, and on the reported regions of genome plasticity. High degrees of sequence similarity were discovered between outbreak isolates collected from recently infected patients, isolates from sinks, an isolate from the sewer, and a historical isolate, suggesting that the ST111 strain has been endemic in the hospital for many years. The ability to translate easily from outbreak investigation to detailed genome biology by use of the same data demonstrates the flexibility of WGS application in a clinical setting.

Genome-wide re-sequencing of multidrug-resistant *Mycobacterium leprae* Airaku-3

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Abstract

Genotyping and molecular characterization of drug resistance mechanisms in *Mycobacterium leprae* enables disease transmission and drug resistance trends to be monitored. In the present study, we performed genome-wide analysis of Airaku-3, a multidrug-resistant strain with an unknown mechanism of resistance to rifampicin. We identified 12 unique non-synonymous single-nucleotide polymorphisms (SNPs) including two in the transporter-encoding *ctpC* and *ctpI* genes. In addition, two SNPs were found that improve the resolution of SNP-based genotyping, particularly for Venezuelan and South East Asian strains of *M. leprae*.